SEQUENCE LISTING

<110> Fleckenstein, Annette E.
Hanson, Glen R.

<120> MODULATING VESICULAR MONOAMINE TRANSPORTER TRAFFICKING AND FUNCTION: A NOVEL APPROACH FOR THE TREATMENT OF PARKINSON'S DISEASE

<130> 21101.0031U3

<150> PCT/US03/29668
<151> 2003-09-19

<150> 60/412,439
<151> 2002-09-19

<160> 18

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 515
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note = synthetic construct

<400> 1

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Met Ala Leu Ser Asp Leu Val Leu Leu Arg Trp Leu Arg Asp Ser Arg
 1               5                  10                  15
His Ser Arg Lys Leu Ile Leu Phe Ile Val Phe Leu Ala Leu Leu Leu
            20                  25                  30
Asp Asn Met Leu Leu Thr Val Val Val Pro Ile Ile Pro Ser Tyr Leu
        35                  40                  45
Tyr Ser Ile Lys His Glu Lys Asn Ser Thr Glu Ile Gln Thr Thr Arg
    50                  55                  60
Pro Glu Leu Val Val Ser Thr Ser Glu Ser Ile Phe Ser Tyr Tyr Asn
65                  70                  75                  80
Asn Ser Thr Val Leu Ile Thr Gly Asn Ala Thr Gly Thr Leu Pro Gly
                85                  90                  95
Gly Gln Ser His Lys Ala Thr Ser Thr Gln His Thr Val Ala Asn Thr
            100                 105                 110
Thr Val Pro Ser Asp Cys Pro Ser Glu Asp Arg Asp Leu Leu Asn Glu
        115                 120                 125
Asn Val Gln Val Gly Leu Leu Phe Ala Ser Lys Ala Thr Val Gln Leu
    130                 135                 140
Leu Thr Asn Pro Phe Ile Gly Leu Leu Thr Asn Arg Ile Gly Tyr Pro
145                 150                 155                 160
Ile Pro Met Phe Ala Gly Phe Cys Ile Met Phe Ile Ser Thr Val Met
                165                 170                 175
Phe Ala Phe Ser Ser Ser Tyr Ala Phe Leu Leu Ile Ala Arg Ser Leu
            180                 185                 190
Gln Gly Ile Gly Ser Ser Cys Ser Ser Val Ala Gly Met Gly Met Leu
        195                 200                 205
Ala Ser Val Tyr Thr Asp Asp Glu Glu Arg Gly Asn Ala Met Gly Ile
    210                 215                 220
Ala Leu Gly Gly Leu Ala Met Gly Val Leu Val Gly Pro Pro Phe Gly
225                 230                 235                 240
```

```
Ser Val Leu Tyr Glu Phe Val Gly Lys Thr Ala Pro Phe Leu Val Leu
                245                 250                 255
Ala Ala Leu Val Leu Leu Asp Gly Ala Ile Gln Leu Phe Val Leu Gln
            260                 265                 270
Pro Ser Arg Val Gln Pro Glu Ser Gln Lys Gly Thr Pro Leu Thr Thr
        275                 280                 285
Leu Leu Lys Asp Pro Tyr Ile Leu Ile Ala Ala Gly Ser Ile Cys Phe
    290                 295                 300
Ala Asn Met Gly Ile Ala Met Leu Glu Pro Ala Leu Pro Ile Trp Met
305                 310                 315                 320
Met Glu Thr Met Cys Ser Arg Lys Trp Gln Leu Gly Val Ala Phe Leu
                325                 330                 335
Pro Ala Ser Ile Ser Tyr Leu Ile Gly Thr Asn Ile Phe Gly Ile Leu
            340                 345                 350
Ala His Lys Met Gly Arg Trp Leu Cys Ala Leu Leu Gly Met Val Ile
        355                 360                 365
Val Gly Ile Ser Ile Leu Cys Ile Pro Phe Ala Lys Asn Ile Tyr Gly
    370                 375                 380
Leu Ile Ala Pro Asn Phe Gly Val Gly Phe Ala Ile Gly Met Val Asp
385                 390                 395                 400
Ser Ser Met Met Pro Ile Met Gly Tyr Leu Val Asp Leu Arg His Val
                405                 410                 415
Ser Val Tyr Gly Ser Val Tyr Ala Ile Ala Asp Val Ala Phe Cys Met
            420                 425                 430
Gly Tyr Ala Ile Gly Pro Ser Ala Gly Gly Ala Ile Ala Lys Ala Ile
        435                 440                 445
Gly Phe Pro Trp Leu Met Thr Ile Ile Gly Ile Ile Asp Ile Ala Phe
    450                 455                 460
Ala Pro Leu Cys Phe Phe Leu Arg Ser Pro Pro Ala Lys Glu Glu Lys
465                 470                 475                 480
Met Ala Ile Leu Met Asp His Asn Cys Pro Ile Lys Thr Lys Met Tyr
                485                 490                 495
Thr Gln Asn Asn Val Gln Ser Tyr Pro Ile Gly Asp Asp Glu Glu Ser
            500                 505                 510
Glu Ser Asp
        515
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<210> 2
<211> 1548
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 2

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atggccctga gcgatctggt gctgctgcga tggctgcggg acagccgcca ctcgcgcaaa      60
ctgatcctgt tcatcgtgtt ccttgcgctg ctgctggaca acatgctgct caccgtcgtg     120
gttcccatca tccccagcta tctgtacagc attaagcatg agaaaaactc tacggaaatc     180
cagaccacca gaccagagct cgtggtctcc acctccgaaa gcatcttctc ttactataac     240
aactctactg tgttgatcac cgggaatgcc actgggactc ttccaggagg gcagtcacac     300
aaggctacca gcacacagca cactgtggct aacaccactg tcccttcgga ctgtcccagt     360
gaagacagag accttctgaa tgagaatgtg caagttgggc tgctgtttgc ctccaaagcc     420
actgtccagc tcctcactaa cccattcata ggacttctga ccaacagaat tggctatcca     480
attcccatgt ttgccggctt ctgcatcatg tttatctcaa cagttatgtt tgccttctcc     540
agcagctatg ccttcctgct gatcgccagg tcccttcagg gaattggctc ctcctgctca     600
tccgtggctg ggatgggtat gctggccagc gtgtacacag atgatgagga gaggggaac      660
gccatgggca ttgctttggg tggcctggcc atgggagtct tagtgggacc ccccttcggg     720
agtgtgctct atgagtttgt ggggaagaca gctcccttcc tggtgctagc tgccttggtg     780
ctcttggatg gggctattca gctctttgtg ctccagccgt cccgagtaca gccagagagt     840
```

```
cagaagggga cacctctaac gaccttgctg aaggatccat acatcctcat cgctgcaggc     900
tccatctgct ttgcaaacat ggggatagcc atgctggagc ccgccctgcc catctggatg     960
atggagacca tgtgttcccg aaagtggcag ctgggcgttg ctttcctccc ggcgagcatc    1020
tcttatctca ttggaaccaa tatttttggg atacttgcac acaaaatggg aaggtggcta    1080
tgtgctcttc tgggaatggt aattgttgga atcagcattt tatgcatccc ctttgcaaaa    1140
aatatctatg gactcatcgc tcccaacttt ggagttggtt ttgcaattgg gatggtggac    1200
tcctctatga tgcctatcat gggctacctg gttgacctgc ggcatgtgtc tgtctatggg    1260
agtgtttatg ccattgcaga cgtggccttt tgtatgggct atgctatcgg tccctctgct    1320
ggtggtgcca tcgcaaaggc aattggcttt ccttggctta tgacaattat tgggataatt    1380
gatatcgctt ttgctccact ctgctttttc cttcgaagtc cacctgctaa ggaggaaaaa    1440
atggctatcc tcatggacca caactgtccc attaaaacaa agatgtacac tcagaataat    1500
gtccagtcat atcccatcgg tgatgatgaa gaatctgaaa gtgactga                  1548
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<210> 3
<211> 514
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 3

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Met Ala Leu Ser Glu Leu Ala Leu Val Arg Trp Leu Gln Glu Ser Arg
 1               5                  10                  15
His Ser Arg Lys Leu Ile Leu Phe Ile Val Phe Leu Ala Leu Leu Leu
            20                  25                  30
Asp Asn Met Leu Leu Thr Val Val Val Pro Ile Ile Pro Ser Tyr Leu
        35                  40                  45
Tyr Ser Ile Lys His Glu Lys Asn Ala Thr Glu Ile Gln Thr Ala Arg
    50                  55                  60
Pro Val His Thr Ala Ser Ile Ser Asp Ser Phe Gln Ser Ile Phe Ser
65                  70                  75                  80
Tyr Tyr Asp Asn Ser Thr Met Val Thr Gly Asn Ala Thr Arg Asp Leu
                85                  90                  95
Thr Leu His Gln Thr Ala Thr Gln His Met Val Thr Asn Ala Ser Ala
            100                 105                 110
Val Pro Ser Asp Cys Pro Ser Glu Asp Lys Asp Leu Leu Asn Glu Asn
        115                 120                 125
Val Gln Val Gly Leu Leu Phe Ala Ser Lys Ala Thr Val Gln Leu Ile
    130                 135                 140
Thr Asn Pro Phe Ile Gly Leu Leu Thr Asn Arg Ile Gly Tyr Pro Ile
145                 150                 155                 160
Pro Ile Phe Ala Gly Phe Cys Ile Met Phe Val Ser Thr Ile Met Phe
                165                 170                 175
Ala Phe Ser Ser Ser Tyr Ala Phe Leu Leu Ile Ala Arg Ser Leu Gln
            180                 185                 190
Gly Ile Gly Ser Ser Cys Ser Ser Val Ala Gly Met Gly Met Leu Ala
        195                 200                 205
Ser Val Tyr Thr Asp Asp Glu Glu Arg Gly Asn Val Met Gly Ile Ala
    210                 215                 220
Leu Gly Gly Leu Ala Met Gly Val Leu Val Gly Pro Pro Phe Gly Ser
225                 230                 235                 240
Val Leu Tyr Glu Phe Val Gly Lys Thr Ala Pro Phe Leu Val Leu Ala
                245                 250                 255
Ala Leu Val Leu Leu Asp Gly Ala Ile Gln Leu Phe Val Leu Gln Pro
            260                 265                 270
Ser Arg Val Gln Pro Glu Ser Gln Lys Gly Thr Pro Leu Thr Thr Leu
        275                 280                 285
Leu Lys Asp Pro Tyr Ile Leu Ile Ala Ala Gly Ser Ile Cys Phe Ala
    290                 295                 300
```

```
Asn Met Gly Ile Ala Met Leu Glu Pro Ala Leu Pro Ile Trp Met Met
305                 310                 315                 320
Glu Thr Met Cys Ser Arg Lys Trp Gln Leu Gly Val Ala Phe Leu Pro
                325                 330                 335
Ala Ser Ile Ser Tyr Leu Ile Gly Thr Asn Ile Phe Gly Ile Leu Ala
            340                 345                 350
His Lys Met Gly Arg Trp Leu Cys Ala Leu Leu Gly Met Ile Ile Val
        355                 360                 365
Gly Val Ser Ile Leu Cys Ile Pro Phe Ala Lys Asn Ile Tyr Gly Leu
    370                 375                 380
Ile Ala Pro Asn Phe Gly Val Gly Phe Ala Ile Gly Met Val Asp Ser
385                 390                 395                 400
Ser Met Met Pro Ile Met Gly Tyr Leu Val Asp Leu Arg His Val Ser
                405                 410                 415
Val Tyr Gly Ser Val Tyr Ala Ile Ala Asp Val Ala Phe Cys Met Gly
            420                 425                 430
Tyr Ala Ile Gly Pro Ser Ala Gly Gly Ala Ile Ala Lys Ala Ile Gly
        435                 440                 445
Phe Pro Trp Leu Met Thr Ile Ile Gly Ile Ile Asp Ile Leu Phe Ala
    450                 455                 460
Pro Leu Cys Phe Phe Leu Arg Ser Pro Pro Ala Lys Glu Glu Lys Met
465                 470                 475                 480
Ala Ile Leu Met Asp His Asn Cys Pro Ile Lys Thr Lys Met Tyr Thr
                485                 490                 495
Gln Asn Asn Ile Gln Ser Tyr Pro Ile Gly Glu Asp Glu Glu Ser Glu
            500                 505                 510
Ser Asp
```

<210> 4
<211> 1545
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 4

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atggccctga gcgagctggc gctggtccgc tggctgcagg agagccgcca ctcgcggaag      60
ctcatcctgt tcatcgtgtt cctggcgctg ctgctggaca acatgctgct cactgtcgtg     120
gtccccatca tcccaagtta tctgtacagc attaagcatg agaagaatgc tacagaaatc     180
cagacggcca ggccagtgca cactgcctcc atctcagaca gcttccagag catcttctcc     240
tattatgata actcgactat ggtcaccggg aatgctacca gagacctgac acttcatcag     300
accgccacac agcacatggt gaccaacgcg tccgctgttc cttccgactg tcccagtgaa     360
gacaaagacc tcctgaatga aaacgtgcaa gttggtctgt tgtttgcctc gaaagccacc     420
gtccagctca tcaccaaccc tttcatagga ctactgacca acagaattgg ctatccaatt     480
cccatatttg cgggattctg catcatgttt gtctcaacaa ttatgtttgc cttctccagc     540
agctatgcct tcctgctgat tgccaggtcg ctgcagggca tcggctcgtc ctgctcctct     600
gtggctggga tgggcatgct tgccagtgtc tacacagatg atgaagagag aggcaacgtc     660
atgggaatcg ccttgggagg cctggccatg ggggtcttag tgggcccccc cttcgggagt     720
gtgctctatg agtttgtggg gaagacggct ccgttcctgg tgctggccgc cctggtactc     780
ttggatggag ctattcagct ctttgtgctc cagccgtccc gggtgcagcc agagagtcag     840
aaggggacac ccctaaccac gctgctgaag gacccgtaca tcctcattgc tgcaggctcc     900
atctgctttg caaacatggg catcgccatg ctggagccag ccctgcccat ctggatgatg     960
gagaccatgt gttcccgaaa gtggcagctg ggcgttgcct tcttgccagc tagtatctct    1020
tatctcattg gaaccaatat ttttgggata cttgcacaca aaatggggag gtggctttgt    1080
gctcttctgg gaatgataat tgttggagtc agcattttat gtattccatt tgcaaaaaac    1140
atttatggac tcatagctcc gaactttgga gttggttttg caattggaat ggtggattcg    1200
tcaatgatgc ctatcatggg ctacctcgta gacctgcggc acgtgtccgt ctatgggagt    1260
gtgtacgcca ttgcggatgt ggcattttgt atggggtatg ctataggtcc ttctgctggt    1320
```

ggtgctattg caaaggcaat tggatttcca tggctcatga caattattgg gataattgat 1380
attctttttg ccccctctctg ctttttttctt cgaagtccac ctgccaaaga agaaaaaatg 1440
gctattctca tggatcacaa ctgccctatt aaaacaaaaa tgtacactca gaataatatc 1500
cagtcatatc cgataggtga agatgaagaa tctgaaagtg actga 1545

<210> 5
<211> 525
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 5

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Met Leu Arg Thr Ile Leu Asp Ala Pro Gln Arg Leu Leu Lys Glu Gly
 1               5                  10                  15
Arg Ala Ser Arg Gln Leu Val Leu Val Val Val Phe Val Ala Leu Leu
            20                  25                  30
Leu Asp Asn Met Leu Phe Thr Val Val Val Pro Ile Val Pro Thr Phe
        35                  40                  45
Leu Tyr Asp Met Glu Phe Lys Glu Val Asn Ser Ser Leu His Leu Gly
    50                  55                  60
His Ala Gly Ser Ser Pro His Ala Leu Ala Ser Pro Ala Phe Ser Thr
65                  70                  75                  80
Ile Phe Ser Phe Phe Asn Asn Asn Thr Val Ala Val Glu Glu Ser Val
                85                  90                  95
Pro Ser Gly Ile Ala Trp Met Asn Asp Thr Ala Ser Thr Ile Pro Pro
            100                 105                 110
Pro Ala Thr Glu Ala Ile Ser Ala His Lys Asn Asn Cys Leu Gln Gly
        115                 120                 125
Thr Gly Phe Leu Glu Glu Glu Ile Thr Arg Val Gly Val Leu Phe Ala
    130                 135                 140
Ser Lys Ala Val Met Gln Leu Leu Val Asn Pro Phe Val Gly Pro Leu
145                 150                 155                 160
Thr Asn Arg Ile Gly Tyr His Ile Pro Met Phe Ala Gly Phe Val Ile
                165                 170                 175
Met Phe Leu Ser Thr Val Met Phe Ala Phe Ser Gly Thr Tyr Thr Leu
            180                 185                 190
Leu Phe Val Ala Arg Thr Leu Gln Gly Ile Gly Ser Ser Phe Ser Ser
        195                 200                 205
Val Ala Gly Leu Gly Met Leu Ala Ser Val Tyr Thr Asp Asp His Glu
    210                 215                 220
Arg Gly Arg Ala Met Gly Thr Ala Leu Gly Gly Leu Ala Leu Gly Leu
225                 230                 235                 240
Leu Val Gly Ala Pro Phe Gly Ser Val Met Tyr Glu Phe Val Gly Lys
                245                 250                 255
Ser Ala Pro Phe Leu Ile Leu Ala Phe Leu Ala Leu Leu Asp Gly Ala
            260                 265                 270
Leu Gln Leu Cys Ile Leu Gln Pro Ser Lys Val Ser Pro Glu Ser Ala
        275                 280                 285
Lys Gly Thr Pro Leu Phe Met Leu Leu Lys Asp Pro Tyr Ile Leu Val
    290                 295                 300
Ala Ala Gly Ser Ile Cys Phe Ala Asn Met Gly Val Ala Ile Leu Glu
305                 310                 315                 320
Pro Thr Leu Pro Ile Trp Met Met Gln Thr Met Cys Ser Pro Lys Trp
                325                 330                 335
Gln Leu Gly Leu Ala Phe Leu Pro Ala Ser Val Ser Tyr Leu Ile Gly
            340                 345                 350
Thr Asn Leu Phe Gly Val Leu Ala Asn Lys Met Gly Arg Trp Leu Cys
        355                 360                 365
```

```
Ser Leu Ile Gly Met Leu Val Val Gly Thr Ser Leu Leu Cys Val Pro
    370                 375                 380
Leu Ala His Asn Ile Phe Gly Leu Ile Gly Pro Asn Ala Gly Leu Gly
385                 390                 395                 400
Leu Ala Ile Gly Met Val Asp Ser Ser Met Met Pro Ile Met Gly His
                405                 410                 415
Leu Val Asp Leu Arg His Thr Ser Val Tyr Gly Ser Val Tyr Ala Ile
            420                 425                 430
Ala Asp Val Ala Phe Cys Met Gly Phe Ala Ile Gly Pro Ser Thr Gly
        435                 440                 445
Gly Ala Ile Val Lys Ala Ile Gly Phe Pro Trp Leu Met Val Ile Thr
    450                 455                 460
Gly Val Ile Asn Ile Val Tyr Ala Pro Leu Cys Tyr Tyr Leu Arg Ser
465                 470                 475                 480
Pro Pro Ala Lys Glu Glu Lys Leu Ala Ile Leu Ser Gln Asp Cys Pro
                485                 490                 495
Met Glu Thr Arg Met Tyr Ala Thr Gln Lys Pro Thr Lys Glu Phe Pro
            500                 505                 510
Leu Gly Glu Asp Ser Asp Glu Glu Pro Asp His Glu Glu
        515                 520                 525
```

<210> 6
<211> 1578
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 6

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atgctccgga ccattctgga tgctccccag cggttgctga aggaggggag agcgtcccgg      60
cagctggtgc tggtggtggt attcgtcgct ttgctcctgg acaacatgct gtttactgtg     120
gtggtgccaa ttgtgcccac cttcctatat gacatggagt tcaaagaagt caactcttct     180
ctgcacctcg gccatgccgg aagttcccca catgccctcg cctctcctgc cttttccacc     240
atcttctcct tcttcaacaa caacaccgtg gctgttgaag aaagcgtacc tagtggaata     300
gcatggatga atgacactgc cagcaccatc ccacctccag ccactgaagc catctcagct     360
cataaaaaca actgcttgca aggcacaggt ttcttggagg aagagattac ccgggtcggg     420
gttctgtttg cttcaaaggc tgtgatgcaa cttctggtca acccattcgt gggccctctc     480
accaacagga ttggatatca tatccccatg tttgctggct ttgttatcat gtttctctcc     540
acagttatgt ttgctttttc tgggacctat actctactct ttgtggcccg aacccttcaa     600
ggcattggat cttcattttc atctgttgca ggtcttggaa tgctggccag tgtctacact     660
gatgaccatg agagaggacg agccatggga actgctctgg ggggcctggc cttggggttg     720
ctggtgggag ctccctttgg aagtgtaatg tacgagtttg ttgggaagtc tgcacccttc     780
ctcatcctgg ccttcctggc actactggat ggagcactcc agctttgcat cctacagcct     840
tccaaagtct ctcctgagag tgccaagggg actcccctct ttatgcttct caaagaccct     900
tacatcctgg tggctgcagg gtccatctgc tttgccaaca tgggggtggc catcctggag     960
cccacactgc ccatctggat gatgcagacc atgtgctccc ccaagtggca gctgggtcta    1020
gctttcttgc ctgccagtgt gtcctacctc attggcacca acctctttgg tgtgttggcc    1080
aacaagatgg gtcggtggct gtgttcccta atcgggatgc tggtagtagg taccagcttg    1140
ctctgtgttc ctctggctca caatattttt ggtctcattg gccccaatgc agggcttggc    1200
cttgccatag gcatggtgga ttcttctatg atgcccatca tggggcacct ggtggatcta    1260
cgccacacct cggtgtatgg gagtgtctac gccatcgctg atgtggcttt ttgcatgggc    1320
tttgctatag gtccatccac cggtggtgcc attgtaaagg ccatcggttt tccctggctc    1380
atggtcatca ctggggtcat caacatcgtc tatgctccac tctgctacta cctgcggagc    1440
cccccggcaa aggaagagaa gcttgctatt ctgagtcagg actgccccat ggagacccgg    1500
atgtatgcaa cccagaagcc cacgaaggaa tttcctctgg gggaggacag tgatgaggag    1560
cctgaccatg aggagtag                                                  1578
```

<210> 7
<211> 446

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 7

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Met Arg Thr Leu Asn Thr Ser Ala Met Asp Gly Thr Gly Leu Val Val
 1               5                  10                  15
Glu Arg Asp Phe Ser Val Arg Ile Leu Thr Ala Cys Phe Leu Ser Leu
            20                  25                  30
Leu Ile Leu Ser Thr Leu Leu Gly Asn Thr Leu Val Cys Ala Ala Val
        35                  40                  45
Ile Arg Phe Arg His Leu Arg Ser Lys Val Thr Asn Phe Phe Val Ile
    50                  55                  60
Ser Leu Ala Val Ser Asp Leu Leu Val Ala Val Leu Val Met Pro Trp
65                  70                  75                  80
Lys Ala Val Ala Glu Ile Ala Gly Phe Trp Pro Phe Gly Ser Phe Cys
                85                  90                  95
Asn Ile Trp Val Ala Phe Asp Ile Met Cys Ser Thr Ala Ser Ile Leu
            100                 105                 110
Asn Leu Cys Val Ile Ser Val Asp Arg Tyr Trp Ala Ile Ser Ser Pro
        115                 120                 125
Phe Arg Tyr Glu Arg Lys Met Thr Pro Lys Ala Ala Phe Ile Leu Ile
    130                 135                 140
Ser Val Ala Trp Thr Leu Ser Val Leu Ile Ser Phe Ile Pro Val Gln
145                 150                 155                 160
Leu Ser Trp His Lys Ala Lys Pro Thr Ser Pro Ser Asp Gly Asn Ala
                165                 170                 175
Thr Ser Leu Ala Glu Thr Ile Asp Asn Cys Asp Ser Ser Leu Ser Arg
            180                 185                 190
Thr Tyr Ala Ile Ser Ser Ser Val Ile Ser Phe Tyr Ile Pro Val Ala
        195                 200                 205
Ile Met Ile Val Thr Tyr Thr Arg Ile Tyr Arg Ile Ala Gln Lys Gln
    210                 215                 220
Ile Arg Arg Ile Ala Ala Leu Glu Arg Ala Ala Val His Ala Lys Asn
225                 230                 235                 240
Cys Gln Thr Thr Thr Gly Asn Gly Lys Pro Val Glu Cys Ser Gln Pro
                245                 250                 255
Glu Ser Ser Phe Lys Met Ser Phe Lys Arg Glu Thr Lys Val Leu Lys
            260                 265                 270
Thr Leu Ser Val Ile Met Gly Val Phe Val Cys Cys Trp Leu Pro Phe
        275                 280                 285
Phe Ile Leu Asn Cys Ile Leu Pro Phe Cys Gly Ser Gly Glu Thr Gln
    290                 295                 300
Pro Phe Cys Ile Asp Ser Asn Thr Phe Asp Val Phe Val Trp Phe Gly
305                 310                 315                 320
Trp Ala Asn Ser Ser Leu Asn Pro Ile Ile Tyr Ala Phe Asn Ala Asp
                325                 330                 335
Phe Arg Lys Ala Phe Ser Thr Leu Leu Gly Cys Tyr Arg Leu Cys Pro
            340                 345                 350
Ala Thr Asn Asn Ala Ile Glu Thr Val Ser Ile Asn Asn Asn Gly Ala
        355                 360                 365
Ala Met Phe Ser Ser His His Glu Pro Arg Gly Ser Ile Ser Lys Glu
    370                 375                 380
Cys Asn Leu Val Tyr Leu Ile Pro His Ala Val Gly Ser Ser Glu Asp
385                 390                 395                 400
Leu Lys Lys Glu Glu Ala Ala Gly Ile Ala Arg Pro Leu Glu Lys Leu
                405                 410                 415
```

```
Ser Pro Ala Leu Ser Val Ile Leu Asp Tyr Asp Thr Asp Val Ser Leu
            420                 425                 430
Glu Lys Ile Gln Pro Ile Thr Gln Asn Gly Gln His Pro Thr
        435                 440                 445
```

<210> 8
<211> 1341
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 8

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atgaggactc tgaacacctc tgccatggac gggactgggc tggtggtgga gagggacttc      60
tctgttcgta tcctcactgc ctgtttccta tcgctgctca tcctgtccac gctcctgggg     120
aacacgctgg tctgtgctgc cgttatcagg ttccgacacc tgcggtccaa ggtgaccaac     180
ttctttgtca tctccttggc tgtgtcagat ctcttggtgg cagtcctggt catgccctgg     240
aaggcagtgg ctgagattgc tggcttctgg ccctttgggt ccttctgtaa catctgggtg     300
gcctttgaca tcatgtgctc cactgcatcc atcctcaacc tctgtgtgat cagcgtggac     360
aggtattggg ctatctccag ccctttccgg tatgagagaa agatgacccc caaggcagcc     420
ttcatcctga tcagtgtggc atggaccttg tctgtactca tctccttcat cccagtgcag     480
ctcagctggc acaaggcaaa acccacaagc ccctctgatg gaaatgccac ttccctggct     540
gagaccatag acaactgtga ctccagcctc agcaggacat atgccatctc atcctctgta     600
ataagctttt acatccctgt ggccatcatg attgtcacct acaccaggat ctacaggatt     660
gctcagaaac aaatacggcg cattgcggcc ttggagaggg cagcagtcca cgccaagaat     720
tgccagacca ccacaggtaa tggaaagcct gtcgaatgtt ctcaaccgga aagttctttt     780
aagatgtcct tcaaaagaga aactaaagtc ctgaagactc tgtcggtgat catgggtgtg     840
tttgtgtgct gttggctacc tttcttcatc ttgaactgca ttttgccctt ctgtgggtct     900
ggggagacgc agcccttctg cattgattcc aacacctttg acgtgtttgt gtggtttggg     960
tgggctaatt catccttgaa ccccatcatt tatgccttta atgctgattt tcggaaggca    1020
ttttcaaccc tcttaggatg ctacagactt tgccctgcga cgaataatgc catagagacg    1080
gtgagtatca ataacaatgg ggccgcgatg ttttccagcc atcatgagcc acgaggctcc    1140
atctccaagg agtgcaatct ggtttacctg atcccacatg ctgtgggctc ctctgaggac    1200
ctgaaaaagg aggaggcagc tggcatcgcc agacccttgg agaagctgtc cccagcccta    1260
tcggtcatat tggactatga cactgacgtc tctctggaga agatccaacc catcacacaa    1320
aacggtcagc acccaacctg a                                              1341
```

<210> 9
<211> 443
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 9

```
Met Asp Pro Leu Asn Leu Ser Trp Tyr Asp Asp Asp Leu Glu Arg Gln
 1               5                  10                  15
Asn Trp Ser Arg Pro Phe Asn Gly Ser Asp Gly Lys Ala Asp Arg Pro
            20                  25                  30
His Tyr Asn Tyr Tyr Ala Thr Leu Leu Thr Leu Leu Ile Ala Val Ile
        35                  40                  45
Val Phe Gly Asn Val Leu Val Cys Met Ala Val Ser Arg Glu Lys Ala
    50                  55                  60
Leu Gln Thr Thr Thr Asn Tyr Leu Ile Val Ser Leu Ala Val Ala Asp
65                  70                  75                  80
Leu Leu Val Ala Thr Leu Val Met Pro Trp Val Val Tyr Leu Glu Val
                85                  90                  95
```

```
Val Gly Glu Trp Lys Phe Ser Arg Ile His Cys Asp Ile Phe Val Thr
            100                 105                 110
Leu Asp Val Met Met Cys Thr Ala Ser Ile Leu Asn Leu Cys Ala Ile
        115                 120                 125
Ser Ile Asp Arg Tyr Thr Ala Val Ala Met Pro Met Leu Tyr Asn Thr
    130                 135                 140
Arg Tyr Ser Ser Lys Arg Arg Val Thr Val Met Ile Ser Ile Val Trp
145                 150                 155                 160
Val Leu Ser Phe Thr Ile Ser Cys Pro Leu Leu Phe Gly Leu Asn Asn
                165                 170                 175
Ala Asp Gln Asn Glu Cys Ile Ile Ala Asn Pro Ala Phe Val Val Tyr
            180                 185                 190
Ser Ser Ile Val Ser Phe Tyr Val Pro Phe Ile Val Thr Leu Leu Val
        195                 200                 205
Tyr Ile Lys Ile Tyr Ile Val Leu Arg Arg Arg Arg Lys Arg Val Asn
    210                 215                 220
Thr Lys Arg Ser Ser Arg Ala Phe Arg Ala His Leu Arg Ala Pro Leu
225                 230                 235                 240
Lys Gly Asn Cys Thr His Pro Glu Asp Met Lys Leu Cys Thr Val Ile
                245                 250                 255
Met Lys Ser Asn Gly Ser Phe Pro Val Asn Arg Arg Arg Val Glu Ala
            260                 265                 270
Ala Arg Arg Ala Gln Glu Leu Glu Met Glu Met Leu Ser Ser Thr Ser
        275                 280                 285
Pro Pro Glu Arg Thr Arg Tyr Ser Pro Ile Pro Pro Ser His His Gln
    290                 295                 300
Leu Thr Leu Pro Asp Pro Ser His His Gly Leu His Ser Thr Pro Asp
305                 310                 315                 320
Ser Pro Ala Lys Pro Glu Lys Asn Gly His Ala Lys Asp His Pro Lys
                325                 330                 335
Ile Ala Lys Ile Phe Glu Ile Gln Thr Met Pro Asn Gly Lys Thr Arg
            340                 345                 350
Thr Ser Leu Lys Thr Met Ser Arg Arg Lys Leu Ser Gln Gln Lys Glu
        355                 360                 365
Lys Lys Ala Thr Gln Met Leu Ala Ile Val Leu Gly Val Phe Ile Ile
    370                 375                 380
Cys Trp Leu Pro Phe Phe Ile Thr His Ile Leu Asn Ile His Cys Asp
385                 390                 395                 400
Cys Asn Ile Pro Pro Val Leu Tyr Ser Ala Phe Thr Trp Leu Gly Tyr
                405                 410                 415
Val Asn Ser Ala Val Asn Pro Ile Ile Tyr Thr Thr Phe Asn Ile Glu
            420                 425                 430
Phe Arg Lys Ala Phe Leu Lys Ile Leu His Cys
        435                 440
```

<210> 10
<211> 1332
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 10

```
atggatccac tgaatctgtc ctggtatgat gatgatctgg agaggcagaa ctggagccgg      60
cccttcaacg ggtcagacgg gaaggcggac agaccccact acaactacta tgccacactg     120
ctcaccctgc tcatcgctgt cattgtcttc ggcaacgtgc tggtgtgcat ggctgtgtcc     180
cgcgagaagg cgctgcagac caccaccaac tacctgatcg tcagcctcgc agtggccgac     240
ctcctcgtcg ccacactggt catgccctgg gttgtctacc tggaggtggt aggtgagtgg     300
aaattcagca ggattcactg tgacatcttc gtcactctgg acgtcatgat gtgcacggcg     360
```

```
agcatcctga acttgtgtgc catcagcatc gacaggtaca cagctgtggc catgcccatg      420
ctgtacaata cgcgctacag ctccaagcgc cgggtcaccg tcatgatctc catcgtctgg      480
gtcctgtcct tcaccatctc ctgcccactc ctcttcggac tcaataacgc agaccagaac      540
gagtgcatca ttgccaaccc ggccttcgtg gtctactcct ccatcgtctc cttctacgtg      600
cccttcattg tcaccctgct ggtctacatc aagatctaca ttgtcctccg cagacgccgc      660
aagcgagtca acaccaaacg cagcagccga gctttcaggg cccacctgag ggctccacta      720
aagggcaact gtactcaccc cgaggacatg aaactctgca ccgttatcat gaagtctaat      780
gggagtttcc cagtgaacag gcggagagtg gaggctgccc ggcgagccca ggagctggag      840
atggagatgc tctccagcac cagcccaccc gagaggaccc ggtacagccc catcccaccc      900
agccaccacc agctgactct ccccgaccca tcccaccacg gtctccacag cactcccgac      960
agccccgcca aaccagagaa gaatgggcat gccaaagacc accccaagat tgccaagatc     1020
tttgagatcc agaccatgcc caatggcaaa acccggacct ccctcaagac catgagccgt     1080
aggaagctct cccagcagaa ggagaagaaa gccactcaga tgctcgccat tgttctcggc     1140
gtgttcatca tctgctggct gcccttcttc atcacacaca tcctgaacat acactgtgac     1200
tgcaacatcc cgcctgtcct gtacagcgcc ttcacgtggc tgggctatgt caacagcgcc     1260
gtgaacccca tcatctacac caccttcaac attgagttcc gcaaggcctt cctgaagatc     1320
ctccactgct ga                                                        1332

<210> 11
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 11
Met Asp Pro Leu Asn Leu Ser Trp Tyr Asp Asp Asp Leu Glu Arg Gln
 1               5                  10                  15
Asn Trp Ser Arg Pro Phe Asn Gly Ser Glu Gly Lys Ala Asp Arg Pro
            20                  25                  30
His Tyr Asn Tyr Tyr Ala Met Leu Leu Thr Leu Leu Ile Phe Ile Ile
        35                  40                  45
Val Phe Gly Asn Val Leu Val Cys Met Ala Val Ser Arg Glu Lys Ala
    50                  55                  60
Leu Gln Thr Thr Thr Asn Tyr Leu Ile Val Ser Leu Ala Val Ala Asp
65                  70                  75                  80
Leu Leu Val Ala Thr Leu Val Met Pro Trp Val Val Tyr Leu Glu Val
                85                  90                  95
Val Gly Glu Trp Lys Phe Ser Arg Ile His Cys Asp Ile Phe Val Thr
            100                 105                 110
Leu Asp Val Met Met Cys Thr Ala Ser Ile Leu Asn Leu Cys Ala Ile
        115                 120                 125
Ser Ile Asp Arg Tyr Thr Ala Val Ala Met Pro Met Leu Tyr Asn Thr
    130                 135                 140
Arg Tyr Ser Ser Lys Arg Arg Val Thr Val Met Ile Ala Ile Val Trp
145                 150                 155                 160
Val Leu Ser Phe Thr Ile Ser Cys Pro Leu Leu Phe Gly Leu Asn Asn
                165                 170                 175
Thr Asp Gln Asn Glu Cys Ile Ile Ala Asn Pro Ala Phe Val Val Tyr
            180                 185                 190
Ser Ser Ile Val Ser Phe Tyr Val Pro Phe Ile Val Thr Leu Leu Val
        195                 200                 205
Tyr Ile Lys Ile Tyr Ile Val Leu Arg Lys Arg Arg Lys Arg Val Asn
    210                 215                 220
Thr Lys Arg Ser Ser Arg Ala Phe Arg Ala Asn Leu Lys Thr Pro Leu
225                 230                 235                 240
Lys Gly Asn Cys Thr His Pro Glu Asp Met Lys Leu Cys Thr Val Ile
                245                 250                 255
```

```
Met Lys Ser Asn Gly Ser Phe Pro Val Asn Arg Arg Arg Met Asp Ala
            260                 265                 270
Ala Arg Arg Ala Gln Glu Leu Glu Met Glu Met Leu Ser Ser Thr Ser
        275                 280                 285
Pro Pro Glu Arg Thr Arg Tyr Ser Pro Ile Pro Pro Ser His His Gln
    290                 295                 300
Leu Thr Leu Pro Asp Pro Ser His His Gly Leu His Ser Asn Pro Asp
305                 310                 315                 320
Ser Pro Ala Lys Pro Glu Lys Asn Gly His Ala Lys Ile Val Asn Pro
                325                 330                 335
Arg Ile Ala Lys Phe Phe Glu Ile Gln Thr Met Pro Asn Gly Lys Thr
            340                 345                 350
Arg Thr Ser Leu Lys Thr Met Ser Arg Arg Lys Leu Ser Gln Gln Lys
        355                 360                 365
Glu Lys Lys Ala Thr Gln Met Leu Ala Ile Val Leu Gly Val Phe Ile
    370                 375                 380
Ile Cys Trp Leu Pro Phe Phe Ile Thr His Ile Leu Asn Ile His Cys
385                 390                 395                 400
Asp Cys Asn Ile Pro Pro Val Leu Tyr Ser Ala Phe Thr Trp Leu Gly
                405                 410                 415
Tyr Val Asn Ser Ala Val Asn Pro Ile Ile Tyr Thr Thr Phe Asn Ile
            420                 425                 430
Glu Phe Arg Lys Ala Phe Met Lys Ile Leu His Cys
        435                 440
```

<210> 12
<211> 1335
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 12

```
atggatccac tgaacctgtc ctggtacgat gacgatctgg agaggcagaa ctggagccgg      60
cccttcaatg ggtcagaagg gaaggcagac aggccccact acaactacta tgccatgctg     120
ctcaccctcc tcatctttat catcgtcttt ggcaatgtgc tggtgtgcat ggctgtatcc     180
cgagagaagg ctttgcagac caccaccaac tacttgatag tcagccttgc tgtggctgat     240
cttctggtgg ccacactggt aatgccgtgg gttgtctacc tggaggtggt gggtgagtgg     300
aaattcagca ggattcactg tgacatcttt gtcactctgg atgtcatgat gtgcacagca     360
agcatcctga acctgtgtgc catcagcatt gacaggtaca cagctgtggc aatgcccatg     420
ctgtataaca cacgctacag ctccaagcgc cgagttactg tcatgattgc cattgtctgg     480
gtcctgtcct tcaccatctc ctgcccactg ctcttcggac tcaacaatac agaccagaat     540
gagtgtatca ttgccaaccc tgcctttgtg gtctactcct ccattgtctc attctacgtg     600
cccttcatcg tcactctgct ggtctatatc aaaatctaca tcgtcctccg gaagcgccgg     660
aagcgggtca acaccaagcg cagcagtcga gctttcagag ccaacctgaa gacaccactc     720
aagggcaact gtacccaccc tgaggacatg aaactctgca ccgttatcat gaagtctaat     780
gggagtttcc cagtgaacag gcggagaatg gatgctgccc gccgagctca ggagctggaa     840
atggagatgc tgtcaagcac cagtccccca gagaggaccc ggtatagccc catccctccc     900
agtcaccacc agctcactct ccctgatcca tcccaccacg gcctacatag caaccctgac     960
agtcctgcca aaccagagaa gaatgggcac gccaagattg tcaatcccag gattgccaag    1020
ttctttgaga tccagaccat gcccaatggc aaaacccgga cctcccttaa gacgatgagc    1080
cgcagaaagc tctcccagca gaaggagaag aaagccactc agatgcttgc cattgttctc    1140
ggtgtgttca tcatctgctg gctgcccttc ttcatcacgc acatcctgaa tatacactgt    1200
gattgcaaca tcccaccagt cctctacagc gccttcacat ggctgggcta tgtcaacagt    1260
gccgtcaacc ccatcatcta caccaccttc aacatcgagt tccgcaaggc cttcatgaag    1320
atcttgcact gctga                                                    1335
```

<210> 13
<211> 444

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 13

```
Met Asp Pro Leu Asn Leu Ser Trp Tyr Asp Asp Asp Leu Glu Arg Gln
 1               5                  10                  15
Asn Trp Ser Arg Pro Phe Asn Gly Ser Glu Gly Lys Ala Asp Arg Pro
            20                  25                  30
His Tyr Asn Tyr Tyr Ala Met Leu Leu Thr Leu Leu Ile Phe Ile Ile
        35                  40                  45
Val Phe Gly Asn Val Leu Val Cys Met Ala Val Ser Arg Glu Lys Ala
    50                  55                  60
Leu Gln Thr Thr Thr Asn Tyr Leu Ile Val Ser Leu Ala Val Ala Asp
65                  70                  75                  80
Leu Leu Val Ala Thr Leu Val Met Pro Trp Val Val Tyr Leu Glu Val
                85                  90                  95
Val Gly Glu Trp Lys Phe Ser Arg Ile His Cys Asp Ile Phe Val Thr
            100                 105                 110
Leu Asp Val Met Met Cys Thr Ala Ser Ile Leu Asn Leu Cys Ala Ile
        115                 120                 125
Ser Ile Asp Arg Tyr Thr Ala Val Ala Met Pro Met Leu Tyr Asn Thr
    130                 135                 140
Arg Tyr Ser Ser Lys Arg Arg Val Thr Val Met Ile Ala Ile Val Trp
145                 150                 155                 160
Val Leu Ser Phe Thr Ile Ser Cys Pro Leu Leu Phe Gly Leu Asn Asn
                165                 170                 175
Thr Asp Gln Asn Glu Cys Ile Ile Ala Asn Pro Ala Phe Val Val Tyr
            180                 185                 190
Ser Ser Ile Val Ser Phe Tyr Val Pro Phe Ile Val Thr Leu Leu Val
        195                 200                 205
Tyr Ile Lys Ile Tyr Ile Val Leu Arg Lys Arg Arg Lys Arg Val Asn
    210                 215                 220
Thr Lys Arg Ser Ser Arg Ala Phe Arg Ala Asn Leu Lys Thr Pro Leu
225                 230                 235                 240
Lys Gly Asn Cys Thr His Pro Glu Asp Met Lys Leu Cys Thr Val Ile
                245                 250                 255
Met Lys Ser Asn Gly Ser Phe Pro Val Asn Arg Arg Arg Met Asp Ala
            260                 265                 270
Ala Arg Arg Ala Gln Glu Leu Glu Met Glu Met Leu Ser Ser Thr Ser
        275                 280                 285
Pro Pro Glu Arg Thr Arg Tyr Ser Pro Ile Pro Pro Ser His His Gln
    290                 295                 300
Leu Thr Leu Pro Asp Pro Ser His His Gly Leu His Ser Asn Pro Asp
305                 310                 315                 320
Ser Pro Ala Lys Pro Glu Lys Asn Gly His Ala Lys Ile Val Asn Pro
                325                 330                 335
Arg Ile Ala Lys Phe Phe Glu Ile Gln Thr Met Pro Asn Gly Lys Thr
            340                 345                 350
Arg Thr Ser Leu Lys Thr Met Ser Arg Arg Lys Leu Ser Gln Gln Lys
        355                 360                 365
Glu Lys Lys Ala Thr Gln Met Leu Ala Ile Val Leu Gly Val Phe Ile
    370                 375                 380
Ile Cys Trp Leu Pro Phe Phe Ile Thr His Ile Leu Asn Ile His Cys
385                 390                 395                 400
Asp Cys Asn Ile Pro Pro Val Leu Tyr Ser Ala Phe Thr Trp Leu Gly
                405                 410                 415
```

```
Tyr Val Asn Ser Ala Val Asn Pro Ile Ile Tyr Thr Thr Phe Asn Ile
            420                 425                 430
Glu Phe Arg Lys Ala Phe Met Lys Ile Leu His Cys
        435                 440
```

<210> 14
<211> 619
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 14

```
Met Ser Lys Ser Lys Cys Ser Val Gly Pro Met Ser Ser Val Val Ala
 1               5                  10                  15
Pro Ala Lys Glu Pro Asn Ala Val Gly Pro Arg Glu Val Glu Leu Ile
            20                  25                  30
Leu Val Lys Glu Gln Asn Gly Val Gln Leu Thr Asn Ser Thr Leu Ile
        35                  40                  45
Asn Pro Pro Gln Thr Pro Val Glu Val Gln Glu Arg Glu Thr Trp Ser
    50                  55                  60
Lys Lys Ile Asp Phe Leu Leu Ser Val Ile Gly Phe Ala Val Asp Leu
65                  70                  75                  80
Ala Asn Val Trp Arg Phe Pro Tyr Leu Cys Tyr Lys Asn Gly Gly Gly
                85                  90                  95
Ala Phe Leu Val Pro Tyr Leu Leu Phe Met Val Ile Ala Gly Met Pro
            100                 105                 110
Leu Phe Tyr Met Glu Leu Ala Leu Gly Gln Phe Asn Arg Glu Gly Ala
        115                 120                 125
Ala Gly Val Trp Lys Ile Cys Pro Val Leu Lys Gly Val Gly Phe Thr
    130                 135                 140
Val Ile Leu Ile Ser Phe Tyr Val Gly Phe Phe Tyr Asn Val Ile Ile
145                 150                 155                 160
Ala Trp Ala Leu His Tyr Phe Phe Ser Ser Phe Thr Met Asp Leu Pro
                165                 170                 175
Trp Ile His Cys Asn Asn Thr Trp Asn Ser Pro Asn Cys Ser Asp Ala
            180                 185                 190
His Ser Ser Asn Ser Ser Asp Gly Leu Gly Leu Asn Asp Thr Phe Gly
        195                 200                 205
Thr Thr Pro Ala Ala Glu Tyr Phe Glu Arg Gly Val Leu His Leu His
    210                 215                 220
Gln Ser Arg Gly Ile Asp Asp Leu Gly Pro Pro Arg Trp Gln Leu Thr
225                 230                 235                 240
Ala Cys Leu Val Leu Val Ile Val Leu Leu Tyr Phe Ser Leu Trp Lys
                245                 250                 255
Gly Val Lys Thr Ser Gly Lys Val Val Trp Ile Thr Ala Thr Met Pro
            260                 265                 270
Tyr Val Val Leu Thr Ala Leu Leu Leu Arg Gly Val Thr Leu Pro Gly
        275                 280                 285
Ala Met Asp Gly Ile Arg Ala Tyr Leu Ser Val Asp Phe Tyr Arg Leu
    290                 295                 300
Cys Glu Ala Ser Val Trp Ile Asp Ala Ala Thr Gln Val Cys Phe Ser
305                 310                 315                 320
Leu Gly Val Gly Phe Gly Val Leu Ile Ala Phe Ser Ser Tyr Asn Lys
                325                 330                 335
Phe Thr Asn Asn Cys Tyr Arg Asp Ala Ile Ile Thr Thr Ser Ile Asn
            340                 345                 350
Ser Leu Thr Ser Phe Ser Ser Gly Phe Val Val Phe Ser Phe Leu Gly
        355                 360                 365
```

```
Tyr Met Ala Gln Lys His Asn Val Pro Ile Arg Asp Val Ala Thr Asp
    370                 375                 380
Gly Pro Gly Leu Ile Phe Ile Ile Tyr Pro Glu Ala Ile Ala Thr Leu
385                 390                 395                 400
Pro Leu Ser Ser Ala Trp Ala Ala Val Phe Phe Leu Met Leu Leu Thr
                405                 410                 415
Leu Gly Ile Asp Ser Ala Met Gly Gly Met Glu Ser Val Ile Thr Gly
            420                 425                 430
Leu Val Asp Glu Phe Gln Leu Leu His Arg His Arg Glu Leu Phe Thr
        435                 440                 445
Leu Gly Ile Val Leu Ala Thr Phe Leu Leu Ser Leu Phe Cys Val Thr
    450                 455                 460
Asn Gly Gly Ile Tyr Val Phe Thr Leu Leu Asp His Phe Ala Ala Gly
465                 470                 475                 480
Thr Ser Ile Leu Phe Gly Val Leu Ile Glu Ala Ile Gly Val Ala Trp
                485                 490                 495
Phe Tyr Gly Val Gln Gln Phe Ser Asp Asp Ile Lys Gln Met Thr Gly
            500                 505                 510
Gln Arg Pro Asn Leu Tyr Trp Arg Leu Cys Trp Lys Leu Val Ser Pro
        515                 520                 525
Cys Phe Leu Leu Tyr Val Val Val Val Ser Ile Val Thr Phe Arg Pro
    530                 535                 540
Pro His Tyr Gly Ala Tyr Ile Phe Pro Asp Trp Ala Asn Ala Leu Gly
545                 550                 555                 560
Trp Ile Ile Ala Thr Ser Ser Met Ala Met Val Pro Ile Tyr Ala Thr
                565                 570                 575
Tyr Lys Phe Cys Ser Leu Pro Gly Ser Phe Arg Glu Lys Leu Ala Tyr
            580                 585                 590
Ala Ile Thr Pro Glu Lys Asp Arg Gln Leu Val Asp Arg Gly Glu Val
        595                 600                 605
Arg Gln Phe Thr Leu Arg His Trp Leu Leu Val
    610                 615
```

<210> 15
<211> 619
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 15

```
Met Ser Lys Ser Lys Cys Ser Val Gly Pro Met Ser Ser Val Val Ala
 1               5                  10                  15
Pro Ala Lys Glu Ser Asn Ala Val Gly Pro Arg Glu Val Glu Leu Ile
            20                  25                  30
Leu Val Lys Glu Gln Asn Gly Val Gln Leu Thr Asn Ser Thr Leu Ile
        35                  40                  45
Asn Pro Pro Gln Thr Pro Val Glu Ala Gln Glu Arg Glu Thr Trp Ser
    50                  55                  60
Lys Lys Ile Asp Phe Leu Leu Ser Val Ile Gly Phe Ala Val Asp Leu
65                  70                  75                  80
Ala Asn Val Trp Arg Phe Pro Tyr Leu Cys Tyr Lys Asn Gly Gly Gly
                85                  90                  95
Ala Phe Leu Val Pro Tyr Leu Leu Phe Met Val Ile Ala Gly Met Pro
            100                 105                 110
Leu Phe Tyr Met Glu Leu Ala Leu Gly Gln Phe Asn Arg Glu Gly Ala
        115                 120                 125
Ala Gly Val Trp Lys Ile Cys Pro Val Leu Lys Gly Val Gly Phe Thr
    130                 135                 140
```

```
Val Ile Leu Ile Ser Phe Tyr Val Gly Phe Phe Tyr Asn Val Ile Ile
145                 150                 155                 160
Ala Trp Ala Leu His Tyr Phe Phe Ser Ser Phe Thr Met Asp Leu Pro
                165                 170                 175
Trp Ile His Cys Asn Asn Thr Trp Asn Ser Pro Asn Cys Ser Asp Ala
            180                 185                 190
His Ala Ser Asn Ser Ser Asp Gly Leu Gly Leu Asn Asp Thr Phe Gly
        195                 200                 205
Thr Thr Pro Ala Ala Glu Tyr Phe Glu Arg Gly Val Leu His Leu His
    210                 215                 220
Gln Ser Arg Gly Ile Asp Asp Leu Gly Pro Pro Arg Trp Gln Leu Thr
225                 230                 235                 240
Ala Cys Leu Val Leu Val Ile Val Leu Leu Tyr Phe Ser Leu Trp Lys
                245                 250                 255
Gly Val Lys Thr Ser Gly Lys Val Val Trp Ile Thr Ala Thr Met Pro
            260                 265                 270
Tyr Val Val Leu Thr Ala Leu Leu Leu Arg Gly Val Thr Leu Pro Gly
        275                 280                 285
Ala Met Asp Gly Ile Arg Ala Tyr Leu Ser Val Asp Phe Tyr Arg Leu
    290                 295                 300
Cys Glu Ala Ser Val Trp Ile Asp Ala Ala Thr Gln Val Cys Phe Ser
305                 310                 315                 320
Leu Gly Val Gly Phe Gly Val Leu Ile Ala Phe Ser Ser Tyr Asn Lys
                325                 330                 335
Phe Thr Asn Asn Cys Tyr Arg Asp Ala Ile Ile Thr Thr Ser Ile Asn
            340                 345                 350
Ser Leu Thr Ser Phe Ser Ser Gly Phe Val Val Phe Ser Phe Leu Gly
        355                 360                 365
Tyr Met Ala Gln Lys His Asn Val Pro Ile Arg Asp Val Ala Thr Asp
    370                 375                 380
Gly Pro Gly Leu Ile Phe Ile Ile Tyr Pro Glu Ala Ile Ala Thr Leu
385                 390                 395                 400
Pro Leu Ser Ser Ala Trp Ala Ala Val Phe Phe Leu Met Leu Leu Thr
                405                 410                 415
Leu Gly Ile Asp Ser Ala Met Gly Gly Met Glu Ser Val Ile Thr Gly
            420                 425                 430
Leu Val Asp Glu Phe Gln Leu Leu His Arg His Arg Glu Leu Phe Thr
        435                 440                 445
Leu Gly Ile Val Leu Ala Thr Phe Leu Leu Ser Leu Phe Cys Val Thr
    450                 455                 460
Asn Gly Gly Ile Tyr Val Phe Thr Leu Leu Asp His Phe Ala Ala Gly
465                 470                 475                 480
Thr Ser Ile Leu Phe Gly Val Leu Ile Glu Ala Ile Gly Val Ala Trp
                485                 490                 495
Phe Tyr Gly Val Gln Gln Phe Ser Asp Asp Ile Lys Gln Met Thr Gly
            500                 505                 510
Gln Arg Pro Asn Leu Tyr Trp Arg Leu Cys Trp Lys Leu Val Ser Pro
        515                 520                 525
Cys Phe Leu Leu Tyr Val Val Val Val Ser Ile Val Thr Phe Arg Pro
    530                 535                 540
Pro His Tyr Gly Ala Tyr Ile Phe Pro Asp Trp Ala Asn Ala Leu Gly
545                 550                 555                 560
Trp Ile Ile Ala Thr Ser Ser Met Ala Met Val Pro Ile Tyr Ala Thr
                565                 570                 575
Tyr Lys Phe Cys Ser Leu Pro Gly Ser Phe Arg Glu Lys Leu Ala Tyr
            580                 585                 590
Ala Ile Thr Pro Glu Lys Asp His Gln Leu Val Asp Arg Gly Glu Val
        595                 600                 605
Arg Gln Phe Thr Leu Arg His Trp Leu Leu Leu
    610                 615
```

<210> 16
<211> 620
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 16

```
Met Ser Lys Ser Lys Cys Ser Val Gly Leu Met Ser Ser Val Val Ala
 1               5                  10                  15
Pro Ala Lys Glu Pro Asn Ala Val Gly Pro Lys Glu Val Glu Leu Ile
            20                  25                  30
Leu Val Lys Glu Gln Asn Gly Val Gln Leu Thr Ser Ser Thr Leu Thr
        35                  40                  45
Asn Pro Arg Gln Ser Pro Val Glu Ala Gln Asp Arg Glu Thr Trp Gly
    50                  55                  60
Lys Lys Ile Asp Phe Leu Leu Ser Val Ile Gly Phe Ala Val Asp Leu
65                  70                  75                  80
Ala Asn Val Trp Arg Phe Pro Tyr Leu Cys Tyr Lys Asn Gly Gly Gly
                85                  90                  95
Ala Phe Leu Val Pro Tyr Leu Leu Phe Met Val Ile Ala Gly Met Pro
            100                 105                 110
Leu Phe Tyr Met Glu Leu Ala Leu Gly Gln Phe Asn Arg Glu Gly Ala
        115                 120                 125
Ala Gly Val Trp Lys Ile Cys Pro Ile Leu Lys Gly Val Gly Phe Thr
    130                 135                 140
Val Ile Leu Ile Ser Leu Tyr Val Gly Phe Phe Tyr Asn Val Ile Ile
145                 150                 155                 160
Ala Trp Ala Leu His Tyr Leu Phe Ser Ser Phe Thr Thr Glu Leu Pro
                165                 170                 175
Trp Ile His Cys Asn Asn Ser Trp Asn Ser Pro Asn Cys Ser Asp Ala
            180                 185                 190
His Pro Gly Asp Ser Ser Gly Asp Ser Ser Gly Leu Asn Asp Thr Phe
        195                 200                 205
Gly Thr Thr Pro Ala Ala Glu Tyr Phe Glu Arg Gly Val Leu His Leu
    210                 215                 220
His Gln Ser His Gly Ile Asp Asp Leu Gly Pro Pro Arg Trp Gln Leu
225                 230                 235                 240
Thr Ala Cys Leu Val Leu Val Ile Val Leu Leu Tyr Phe Ser Leu Trp
                245                 250                 255
Lys Gly Val Lys Thr Ser Gly Lys Val Val Trp Ile Thr Ala Thr Met
            260                 265                 270
Pro Tyr Val Val Leu Thr Ala Leu Leu Leu Arg Gly Val Thr Leu Pro
        275                 280                 285
Gly Ala Ile Asp Gly Ile Arg Ala Tyr Leu Ser Val Asp Phe Tyr Arg
    290                 295                 300
Leu Cys Glu Ala Ser Val Trp Ile Asp Ala Ala Thr Gln Val Cys Phe
305                 310                 315                 320
Ser Leu Gly Val Gly Phe Gly Val Leu Ile Ala Phe Ser Ser Tyr Asn
                325                 330                 335
Lys Phe Thr Asn Asn Cys Tyr Arg Asp Ala Ile Val Thr Thr Ser Ile
            340                 345                 350
Asn Ser Leu Thr Ser Phe Ser Ser Gly Phe Val Val Phe Ser Phe Leu
        355                 360                 365
Gly Tyr Met Ala Gln Lys His Ser Val Pro Ile Gly Asp Val Ala Lys
    370                 375                 380
Asp Gly Pro Gly Leu Ile Phe Ile Ile Tyr Pro Glu Ala Ile Ala Thr
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Leu Pro Leu Ser Ser Ala Trp Ala Val Val Phe Phe Ile Met Leu Leu
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Thr Leu Gly Ile Asp Ser Ala Met Gly Gly Met Glu Ser Val Ile Thr
            420                 425                 430
Gly Leu Ile Asp Glu Phe Gln Leu Leu His Arg His Arg Glu Leu Phe
        435                 440                 445
Thr Leu Phe Ile Val Leu Ala Thr Phe Leu Leu Ser Leu Phe Cys Val
    450                 455                 460
Thr Asn Gly Gly Ile Tyr Val Phe Thr Leu Leu Asp His Phe Ala Ala
465                 470                 475                 480
Gly Thr Ser Ile Leu Phe Gly Val Leu Ile Glu Ala Ile Gly Val Ala
                485                 490                 495
Trp Phe Tyr Gly Val Gly Gln Phe Ser Asp Asp Ile Gln Gln Met Thr
            500                 505                 510
Gly Gln Arg Pro Ser Leu Tyr Trp Arg Leu Cys Trp Lys Leu Val Ser
        515                 520                 525
Pro Cys Phe Leu Leu Phe Val Val Val Val Ser Ile Val Thr Phe Arg
    530                 535                 540
Pro Pro His Tyr Gly Ala Tyr Ile Phe Pro Asp Trp Ala Asn Ala Leu
545                 550                 555                 560
Gly Trp Val Ile Ala Thr Ser Ser Met Ala Met Val Pro Ile Tyr Ala
                565                 570                 575
Ala Tyr Lys Phe Cys Ser Leu Pro Gly Ser Phe Arg Glu Lys Leu Ala
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<212> DNA
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synthetic construct

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<220>
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